

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 06:11:39 ; Search time 93 Seconds
(without alignments)
897.515 Million cell updates/sec

Title: US-10-616-410-2
Perfect score: 852
Sequence: 1 MADEEKLPPGWEKMRSSG.....GEMSGPVFTDSGIHILRTE 163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance, to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	852	100.0	163	1	PIN1_HUMAN	Q13526 homo sapien
2	814	95.5	165	1	PIN1_MOUSE	Q9qur7 mus musculus
3	753	88.4	159	2	Q919K6	Q919k6 xenopus lae
4	752	88.3	159	2	Q642N3	Q642n3 xenopus tro
5	751	88.1	159	2	Q6DEE1	Q6dee1 xenopus lae
6	748	87.8	158	2	Q6AZR5	Q6aazr5 xenopus lae
7	681	79.9	159	2	Q6P6X1	Q6pbx1 brachydanio
8	491	57.6	191	2	Q7QAB6	Q7qab6 anopheles g
9	456.5	53.6	166	1	DOD DROME	P54353 drosophila
10	436	51.2	168	2	Q9N492	Q9n492 caenorhabdi
11	433.5	50.9	186	2	Q7RVY7	Q7rvy7 neurospora
12	428.5	50.3	182	1	SSP1_NEUCR	O60045 neurospora
13	408.5	47.9	190	2	Q6UAY2	Q6uay2 paracoccidi
14	397	46.6	176	2	O42735	O42735 emericeella
15	388.5	45.6	175	1	PIN1_SCHPO	O74448 schizosacch
16	387	45.4	185	2	Q6CEL8	O6cel8 yarrowia li
17	370	43.4	162	2	Q6CMZ3	Q6cmz3 kluyveromyc
18	369.5	43.4	177	2	Q9C475	Q9c475 candida alb
19	364	42.7	178	2	Q8NJN5	Q8njn5 cryptococcu
20	360	42.3	177	2	Q6BRV8	Q6brv8 debaryomyce
21	356.5	41.8	190	1	ESS1_YEAST	P22696 saccharomyc
22	352	41.3	173	2	Q6FXP9	Q6fxp9 candida gla
23	351.5	41.3	243	2	P90527	P90527 dictyosteli
24	341	40.0	163	2	Q75CN9	Q75cn9 ashbya goss
25	338	39.7	148	2	Q7QAB7	Q7qab7 anopheles g
26	301	35.3	119	1	PIN1_ARATH	Q9sl42 arabidopsis
27	297	34.9	100	1	PINL_HUMAN	O15428 homo sapien
28	296.5	34.8	121	1	PIN1_MALDO	Q94g00 malus domes
29	283	33.2	118	1	PIN1_DIGLA	Q9lek8 digitalis l
30	280	32.9	123	2	Q7XTK0	Q7xtk0 oryza sativ
31	277	32.5	386	2	Q8IRJ5	Q8irj5 drosophila

32	218.5	25.6	150	2	Q8SR55	Q8sr55 encephalito
33	186.5	21.9	90	2	Q6MR41	Q6mr41 bdellovibri
34	186	21.8	629	2	Q72D64	Q72d64 desulfovibr
35	185	21.7	630	2	Q82SU8	Q82su8 nitrosomona
36	184	21.6	321	2	Q74BG7	Q74bg7 geobacter s
37	181	21.2	246	2	Q899G4	Q899g4 clostridium
38	180.5	21.2	292	1	PRSA_BACSU	P24327 bacillus su
39	179.5	21.1	92	2	Q74049	Q74049 cenarchaeum
40	177	20.8	247	2	Q97MB9	Q97mb9 clostridium
41	176	20.7	351	2	Q74AE7	Q74ae7 geobacter s
42	159.5	18.7	148	2	Q6ESK5	Q6esk5 oryza sativ
43	159.5	18.7	317	2	Q6G5U1	Q6g5u1 bartonella
44	158.5	18.6	286	2	Q65LT4	Q65lt4 bacillus li
45	158.5	18.6	317	2	Q6G0Q7	Q6g0q7 bartonella

ALIGNMENTS

RESULT 1
PIN1_HUMAN
ID PIN1_HUMAN STANDARD; PRT; 163 AA.
AC Q13526;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (EC 5.2.1.8)
DE (Rotamase Pin1) (PPIase Pin1).
GN Name=PIN1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96195064; PubMed=8606777; DOI=10.1038/380544a0;
RA Lu K.P., Hanes S.D., Hunter T.;
RT "A human peptidyl-prolyl isomerase essential for regulation of
mitosis.";
RL Nature 380:544-547 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.35 ANGSTROMS).
RX MEDLINE=97344079; PubMed=9200606; DOI=10.1016/S0092-8674(00)80273-1;
RA Ranganathan R., Lu K.P., Hunter T., Noel J.P.;
RT "Structural and functional analysis of the mitotic rotamase Pin1
suggests substrate recognition is phosphorylation dependent.";
RL Cell 89:875-886 (1997).
CC -!- FUNCTION: Essential PPIase that regulates mitosis presumably by
interacting with NIMA and attenuating its mitosis-promoting

Exhib F

CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline (omega=0).

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -1- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.

CC -1- SIMILARITY: Contains 1 WW domain.

CC -----

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CC -----

CC EMBL; AB009691; BAA87037.1; -.

CC EMBL; AB009692; BAA87038.1; -.

CC EMBL; AK003369; BAB22743.1; -.

CC EMBL; AK002665; BAB22270.1; -.

CC PIR; JC7136; JC7136.

CC HSSP; Q13526; 1F8A.

CC MGD; MGI:1346036; Pin1.

CC GO; GO:0042127; P:regulation of cell proliferation; IMP.

CC InterPro; IPR000297; Rotamase.

CC InterPro; IPR001202; WW_Rap5_WWP.

CC Pfam; PF00639; Rotamase; 1.

CC Pfam; PF00397; WW; 1.

CC SMART; SM00456; WW; 1.

CC PROSITE; PS01096; PPIC_PPIASE_1; 1.

CC PROSITE; PS01159; WW_DOMAIN_1; 1.

CC PROSITE; PS01159; WW_DOMAIN_2; 1.

CC PROSITE; PS50020; WW_DOMAIN_2; 1.

CC Cell cycle; Isomerase; Nuclear protein; Rotamase.

KW DOMAIN 5 39 WW.

FT DOMAIN 54 165 PpiC.

FT SEQUENCE 165 AA; 18370 MW; 188E95F009176B1F CRC64;

SQ

Query Match 95.5%; Score 814; DB 1; Length 165;

Best Local Similarity 95.2%; Pred. No. 9.4e-67;

Matches 157; Conservative 3; Mismatches 3; Indels 2; Gaps 1;

QY 1 MADEEKLPPGWEKMRSSGRVYFNHITNASQWERPSGNSSGG--KNGQGEPAVRCS 58

Db 1 MADEEKLPPGWEKMRSSGRVYFNHITNASQWERPSGGSTVGSSKNGQGEPAVRCS 60

QY 59 HLLVKHSQSRPPSSWRQEKITRTKEEALELINGYIQIKSGEEDFESLASQFSDCSSAKA 118

Db 61 HLLVKHSQSRPPSSWRQEKITRTKEEALELINGYIQIKSGEEDFESLASQFSDCSSAKA 120

QY 119 RGDLGAFSRGQMOKPFEDASPALRTGEMSGPVFTDSGIHILRTE 163

Db 121 RGDLPFSPRGQMOKPFEDASPALRTGEMSGPVFTDSGIHILRTE 165

RESULT 3

Q919K6 PRELIMINARY; PRT; 159 AA.

AC Q919K6; (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Prolyl isomerase Pin1.

GN Name=Pin1;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20165035; PubMed=10698738; DOI=10.1126/science.287.5458.1644;

RA Winkler K.B., Swenson K.I., Kornbluth S., Means A.R.;

RT "Requirement of the prolyl isomerase Pin1 for the replication checkpoint."

RL Science 287:1644-1647(2000).

CC -1- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.

DR EMBL; AF239760; AAF43897.1; -.

DR HSSP; Q13526; 1F8A.

DR GO; GO:0016853; F:Isomerase activity; IEA.

DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.

DR GO; GO:0006457; P:protein folding; IEA.

DR InterPro; IPR000297; Rotamase.

DR InterPro; IPR002349; WW.

DR InterPro; IPR001202; WW_Rap5_WWP.

DR Pfam; PF00639; Rotamase; 1.

DR Pfam; PF00397; WW; 1.

DR PRINTS; PR00403; WWDOMAIN.

DR SMART; SM00456; WW; 1.

DR PROSITE; PS01096; PPIC_PPIASE_1; 1.

DR PROSITE; PS01159; PPIC_PPIASE_2; 1.

DR PROSITE; PS01159; WW_DOMAIN_1; 1.

DR PROSITE; PS50020; WW_DOMAIN_2; 1.

KW Isomerase; Rotamase.

SQ SEQUENCE 159 AA; 17671 MW; 4E54F66F16C9DF1C CRC64;

Query Match 88.4%; Score 753; DB 2; Length 159;

Best Local Similarity 87.1%; Pred. No. 3.6e-61;

Matches 142; Conservative 11; Mismatches 6; Indels 4; Gaps 1;

QY 1 MADEEKLPPGWEKMRSSGRVYFNHITNASQWERPSGNSSGGKNGQGEPAVRCSHL 60

Db 1 MADEEKLPPGWEKMRSSGRVYFNHITNASQWERP----IAGKNGQGEPAVRCSHL 56

QY 61 LVKHSQSRPPSSWRQEKITRTKEEALELINGYIQIKSGEEDFESLASQFSDCSSAKAG 120

Db 57 LVKHNQSRPPSSWRQDKITRSKDEALELINGYIQMKSGDEDFESLASQFSDCSSAKAG 116

QY 121 DLGAFSRGQMOKPFEDASPALRTGEMSGPVFTDSGIHILRTE 163

Db 117 DLGSFGKGAMQKPFEDASFALRPGEMSGPVFTDSGIHILRTE 159

RESULT 4

Q642N3 PRELIMINARY; PRT; 159 AA.

AC Q642N3;

DT 25-OCT-2004 (TREMBlrel. 28, Created)

DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)

DE Hypothetical protein.

OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8364;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

Db 126 ALTESDCSSARKRGDLGYFGRGDMQKEFEDAAAFALKPGEISDIVDTASGLHLIERLE 182

RESULT 13

Q6UAY2 PRELIMINARY; PRT; 190 AA.

AC Q6UAY2;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE Peptidyl-prolyl cis/trans isomerase.

OS Paracoccidioides brasiliensis.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Onygenales; mitosporic Onygenales; Paracoccidioides.

OX NCBI_TaxID=121759;

RN [1]

RP SEQUENCE FROM N.A.

RA Domingos F.C., Pereira M., Castro N.S., Felipe M.S.S., Soares C.M.A.,

RA Jesuino R.S.A.;

RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.

DR EMBL; AY374446; AAQ83700.1; -.

DR GO; GO:0016853; F:isomerase activity; IEA.

DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.

DR GO; GO:0006457; P:protein folding; IEA.

DR InterPro; IPR000297; Rotamase.

DR InterPro; IPR001202; WW_Rap5_WWP.

DR Pfam; PF00639; Rotamase; 1.

DR Pfam; PF00397; WW; 1.

DR SMART; SM00456; WW; 1.

DR PROSITE; PS50198; PPIC_PPIASE_2; 1.

DR PROSITE; PS01159; WW_DOMAIN_1; 1.

DR PROSITE; PS50020; WW_DOMAIN_2; 1.

KW Isomerase; Rotamase.

SQ SEQUENCE 190 AA; 20983 MW; 710DCBEFAA9238AE CRC64;

Query Match 47.9%; Score 408.5; DB 2; Length 190;

Best Local Similarity 44.9%; Pred. No. 1.9e-29;

Matches 83; Conservative 24; Mismatches 53; Indels 25; Gaps 1;

QY 4 EEKLPWGWEKMRSSGRVYFNFHITNASQWERPSGNS----- 41

Db 6 ETGLPSGWEVRHSNKNLPYFNPITKESRWEPSPNTDEKLKEYMAQHHSGLAERNNA 65

QY 42 ---SSGGKNGQGEPAVRVCSHLLVKHSQSRPPSSWRQEKITRTKEALELINGYIQIKS 98

Db 66 TGVTSAGVSSSADGKIPASHLLIKHQGSRPPSSWRQEAITRSKEALBILRRHESIRS 125

QY 99 GEEDFESLASQFSDCSSAKARGDLGAFSRGQMKPFEDASFALRTGEMSGPVFTDSGIHI 158

Db 126 GEKTLGDIAMSESDCSSARKRGDLGFFGRGEMQAEFEAAFALEPQGVSGIVETASGVHL 185

QY 159 ILRTE 163

Db 186 IERLQ 190

RESULT 14

O42735 PRELIMINARY; PRT; 176 AA.

AC O42735;

DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Peptidyl-prolyl cis/trans isomerase.

GN Name=pina;

OS Emericella nidulans (Aspergillus nidulans).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; Emericella.

OX NCBI_TaxID=162425;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=R153;

RX MEDLINE=98151356; PubMed=9482729; DOI=10.1093/emboj/17.5.1315;

RA Crenshaw D.G., Yang J., Means A.R., Kornbluth S.;

RT "The mitotic peptidyl-prolyl isomerase, Pin1, interacts with Cdc25 and Plx1.";

RL EMBO J. 17:1315-1327(1998).

CC -1- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.

DR EMBL; AF035768; AAC49984.1; -.

DR HSSP; Q13526; 1F8A.

DR GO; GO:0016853; F:isomerase activity; IEA.

DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.

DR GO; GO:0006457; P:protein folding; IEA.

DR InterPro; IPR000297; Rotamase.

DR InterPro; IPR001202; WW_Rap5_WWP.

DR Pfam; PF00639; Rotamase; 1.

DR Pfam; PF00397; WW; 1.

DR SMART; SM00456; WW; 1.

DR PROSITE; PS50198; PPIC_PPIASE_2; 1.

DR PROSITE; PS01159; WW_DOMAIN_1; 1.

DR PROSITE; PS50020; WW_DOMAIN_2; 1.

KW Isomerase; Rotamase.

SQ SEQUENCE 176 AA; 20038 MW; 1D1E8376239E1309 CRC64;

Query Match 46.6%; Score 397; DB 2; Length 176;

Best Local Similarity 48.0%; Pred. No. 1.9e-28;

Matches 82; Conservative 24; Mismatches 51; Indels 14; Gaps 2;

QY 7 LPPGWKEKMRSSGRVYFNFHITNASQWERPSGNS-----SSGGKNGQGEPA-- 53

Db 6 LPAGWEVRHSNKNLPYFNPATRESRWEPADTDMETLKNMATYHSGAATHEAPSQE 65

QY 54 -RVRCSHLLVKHSQSRPPSSWRQEKITRTKEALELINGYIQIKSGEEDFESLASQFSD 112

Db 66 GKIRCSHLLVKHDSRRPSSWRQEAITRTKEAREILRGHQRIMRGEIRLGLAMSESD 125

QY 113 CSSAKARGDLGAFSRGQMKPFEDASFALRTGEMSGPVFTDSGIHIILRTE 163

Db 126 CSSARKRGDLGFFGRGEMQKEFEAAFALEPQGVSDIVESGSLHLIERLQ 176

RESULT 15

PIN1_SCHPO STANDARD; PRT; 175 AA.

AC O74448;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Peptidyl-prolyl cis-trans isomerase pin1 (RC 5.2.1.8).

GN Name=pin1; ORFNames=SPCC16C4.03;

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

Search completed: April 6, 2005, 06:27:26
Job time : 95 secs